

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Regucalcin gene-transferred non-human animals

<130> YG2002-18PCT

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<150> JP P2001-287698

<151> 2001-9-20

<150> JP P2002-177666

<151> 2002-6-18

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 900

<212> DNA

<213> Rattus norvegicus

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<221> CDS

<222> (1)..(900)

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10

15

ggg gag tcc cct gtg tgg gag gag gca tca aag tgt ctg ctg ttt gta 96

Gly	Glu	Ser	Pro	Val	Trp	Glu	Glu	Ala	Ser	Lys	Cys	Leu	Leu	Phe	Val	
			20					25					30			
gac atc cct tca aag act gtc tgc cga tgg gat tcg atc agc aat cga															144	
Asp Ile Pro Ser Lys Thr Val Cys Arg Trp Asp Ser Ile Ser Asn Arg																
			35					40					45			
gtg cag cga gtt ggt gta gat gcc cca gtc agt tca gtg gca ctt cga															192	
Val Gln Arg Val Gly Val Asp Ala Pro Val Ser Ser Val Ala Leu Arg																
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cag tca gga ggc tat gtt gcc acc att gga acc aag ttc tgt gct ttt															240	
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu																
			65					70					75			80
aac tgg gaa gat caa tca gta ttt atc cta gcc atg gtg gat gaa gat															288	
Asn Trp Glu Asp Gln Ser Val Phe Ile Leu Ala Met Val Asp Glu Asp																
			85					90					95			
aag aaa aac aat cga ttc aat gat ggg aag gtg gat cct gct ggg aga															336	
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg																
			100					105					110			
tac ttt gct ggt acc atg gct gag gaa acc gcc cca gct gtt ctg gag															384	
Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu																
			115					120					125			
cgg cac caa ggg tcc ttg tac tcc ctt ttt cct gat cac agt gtg aag															432	
Arg His Gln Gly Ser Leu Tyr Ser Leu Phe Pro Asp His Ser Val Lys																
			130					135					140			
aaa tac ttt aac caa gtg gat atc tcc aat ggt ttg gat tgg tcc ctg															480	
Lys Tyr Phe Asn Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu																
			145					150					155			160
gac cat aaa atc ttc tac tac att gac agc ctg tcc tac act gtg gat															528	

Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Thr Val Asp			
165	170	175	
gcc ttt gac tat gac ctg cca aca gga cag att tcc aac cgc agg act 576			
Ala Phe Asp Tyr Asp Leu Pro Thr Gly Gln Ile Ser Asn Arg Arg Thr			
180	185	190	
gtt tac aag atg gaa aaa gat gaa caa atc cca gat gga atg tgc att 624			
Val Tyr Lys Met Glu Lys Asp Glu Gln Ile Pro Asp Gly Met Cys Ile			
195	200	205	
gat gtt gag ggg aag ctt tgg gtg gcc tgt tac aat gga gga aga gta 672			
Asp Val Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val			
210	215	220	
att cgc cta gat cct gag aca ggg aaa aga ctg caa act gtg aag ttg 720			
Ile Arg Leu Asp Pro Glu Thr Gly Lys Arg Leu Gln Thr Val Lys Leu			
225	230	235	240
cct gtt gat aaa aca act tca tgc tgc ttt gga ggg aag gat tac tct 768			
Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser			
245	250	255	
gaa atg tac gtg aca tgt gcc agg gat ggg atg agc gcc gaa ggt ctt 816			
Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu			
260	265	270	
ttg agg cag cct gat gct ggt aac att ttc aag ata aca ggt ctt ggg 864			
Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly			
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<400> 2

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Asp	Ile	Pro	Ser	Lys	Thr	Val	Cys	Arg	Trp	Asp	Ser	Ile	Ser	Asn	Arg
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Gln	Ser	Gly	Gly	Tyr	Val	Ala	Thr	Ile	Gly	Thr	Lys	Phe	Cys	Ala	Leu
					65			70			75			80	
Asn	Trp	Glu	Asp	Gln	Ser	Val	Phe	Ile	Leu	Ala	Met	Val	Asp	Glu	Asp
					85				90			95			
Lys	Lys	Asn	Asn	Arg	Phe	Asn	Asp	Gly	Lys	Val	Asp	Pro	Ala	Gly	Arg
					100				105			110			
Tyr	Phe	Ala	Gly	Thr	Met	Ala	Glu	Glu	Thr	Ala	Pro	Ala	Val	Leu	Glu
					115			120			125				
Arg	His	Gln	Gly	Ser	Leu	Tyr	Ser	Leu	Phe	Pro	Asp	His	Ser	Val	Lys
					130			135			140				
Lys	Tyr	Phe	Asn	Gln	Val	Asp	Ile	Ser	Asn	Gly	Leu	Asp	Trp	Ser	Leu
					145			150			155			160	
Asp	His	Lys	Ile	Phe	Tyr	Tyr	Ile	Asp	Ser	Leu	Ser	Tyr	Thr	Val	Asp
					165				170			175			
Ala	Phe	Asp	Tyr	Asp	Leu	Pro	Thr	Gly	Gln	Ile	Ser	Asn	Arg	Arg	Thr
					180				185			190			
Val	Tyr	Lys	Met	Glu	Lys	Asp	Glu	Gln	Ile	Pro	Asp	Gly	Met	Cys	Ile
					195			200			205				
Asp	Val	Glu	Gly	Lys	Leu	Trp	Val	Ala	Cys	Tyr	Asn	Gly	Gly	Arg	Val
					210			215			220				
Ile	Arg	Leu	Asp	Pro	Glu	Thr	Gly	Lys	Arg	Leu	Gln	Thr	Val	Lys	Leu
					225			230			235			240	

Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asp Tyr Ser
245 250 255
Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Ser Ala Glu Gly Leu
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Leu Arg Gln Pro Asp Ala Gly Asn Ile Phe Lys Ile Thr Gly Leu Gly
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Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
290 295

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer huRC-1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer huRC-2

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23